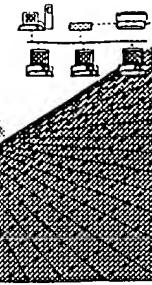


M. Park

1646

BIOTECHNOLOGY
SYSTEMS
BRANCH



#30/52
9-13-01

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/816,010
Source: 01PF
Date Processed by STIC: 6/15/2001

RECEIVED

AUG 27 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

AUG 27 2001

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ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 08/816,010

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220> Sequence(s) 65 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Re-run

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:04

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

Does Not Comply
Corrected Diskette Needed
P. 6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:04

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

59 gatgctttgg aggagcagct gagaaacaat caccgggtgc cggtcgctc aagaagttct 1800
60 ccatgcccga tggctcgca cgtctgtttc cttccagaa gaagcacccc tcgcaggatc 1860
61 tggagcgcaa gttgtccgtg gtctcggtac cggagggtgt catctcgag gaagccatg 1920
62 ccccgctgga ctactacatc aacacggtaa cggccgcctc cagtcaatcc tatttgcga 1980
63 acggacgcgg tccgcaccg cccttcgaat cgaatggcag cttggccagc ggcggcggcg 2040
64 ggctaacgaa catggcttc cagatggagg atggagcaac cccgcccattcg gcattggcg 2100
65 gtggagccta tcaacgcaag gcccgtgctg gcaagcggcg acgegagagc atctacaccc 2160
66 agaatcaagc cccatccgct cggccggggca gcatgtatcc gcccggccgc caccgccttgg 2220
67 cccagatgca gatgcgacgc ggcagcttgg caaccagtgg ctctggatcg gcccgcattgg 2280
68 cgcagtgcc ggcgcgtcg tcccaagctac agcatcggca tcatcgctga 2340
69 cctctgctcc ggcggcaagc agcatattct cggttacctc cggaaaggat atgaatgtgc 2400
70 tggagcagac gaccattgcg gatctgattc gtgcgctcga 2441
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 618
75 <212> TYPE: PRT
76 <213> ORGANISM: Drosophila melanogaster
78 <400> SEQUENCE: 2
79 Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr
80 1 5 10 15
82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
83 20 25 30
85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
86 35 40 45
88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Gln Asp Glu
89 50 55 60
91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
92 65 70 75 80
94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
95 85 90 95
97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
98 100 105 110
100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
101 115 120 125
103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
104 130 135 140
106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
107 145 150 155 160
109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
110 165 170 175
112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
113 180 185 190
115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
116 195 200 205
118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Ile Gly Phe Gly Asp Tyr
119 210 215 220
121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
122 225 230 235 240
124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
125 245 250 255

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:04

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
 128 260 265 270
 130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
 131 275 280 285
 133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
 134 290 295 300
 136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
 137 305 310 315 320
 139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
 140 325 330 335
 142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
 143 340 345 350
 145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
 146 355 360 365
 148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
 149 370 375 380
 151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
 152 385 390 395 400
 154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
 155 405 410 415
 157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
 158 420 425 430
 160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
 161 435 440 445
 163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
 164 450 455 460
 166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
 167 465 470 475 480
 169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
 170 485 490 495
 172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
 173 500 505 510
 175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
 176 515 520 525
 178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
 179 530 535 540
 181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
 182 545 550 555 560
 184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
 185 565 570 575
 187 Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
 188 580 585 590
 190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
 191 595 600 605
 193 Met Ala Ala Trp Pro Ala Ala Ala Gly
 194 610 615
 197 <210> SEQ ID NO: 3
 198 <211> LENGTH: 1011
 199 <212> TYPE: DNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:04

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

200 <213> ORGANISM: *Caenorhabditis elegans*
 202 <400> SEQUENCE: 3
 203 atgtccgatc ägctgttgt cgcatggag aagtattct tgacgagtaa cgaggtaag 60
 204 aagaatgcag caacggägac atggacattt tcatcgcca ttttcttgc cgttaaccgtc 120
 205 gtcactacca tcggatacgg taatccagtt ccagtacaa acattggacg gatatggtgt 180
 206 atattgttct ccttgcttgg aatacctcta acactggta ccatcgctga cttggcagg 240
 207 aaattcctat ctgaacatct tgtttgggtg tatggaaact atttgaattt aaaaatatctc 300
 208 atattgtcac gacatcgaaa agaacggaga gagcacgtt gtgagcactg \tcacagtcat 360
 209 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
 210 attctgatag tatatacagc gtttggcggt gtcctaattgt caaaaattaga gccgtggct 480
 211 ttcttcactt cattctactg gtccttcatt acaatgacta ctgtcggtt tggcgacttg 540
 212 atgcccagaa gggacggata catgtatatac atattgtct atatcattt agttaaattt 600
 213 tcaatgaaaa aaaaacaaaa attcaaaata tttttaggtc ttgcaataac tacaatgtgc 660
 214 attgatttgg taggagtaca gtatattcga aagattcatt atttcggaaag aaaaattcaa 720
 215 gacgctagat ctgcattggc ggtttagga ggaaaggtag tccttgatc agaactctac 780
 216 gcaaatttaa tgcaaaagcg agtcgtaac atgtcccgag aagctttat agtggagaat 840
 217 ctctatgttt ccaaacacat cataccattc ataccaactg atatccgatg tattcgatat 900
 218 attgatcaaa ctgcccgtgc tgctaccatt tccacgtcat cgtctgcaat tgatätgcaa 960
 219 agttgtagat tttgtcatc aagatattct ctcaatcgat cattcaaata g 1011
 222 <210> SEQ ID NO: 4
 223 <211> LENGTH: 336
 224 <212> TYPE: PRT
 225 <213> ORGANISM: *Drosophila melanogaster*
 227 <400> SEQUENCE: 4
 228 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
 229 1 5 10 15
 231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
 232 20 25 30
 234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
 235 35 40 45
 237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 238 50 55 60
 240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
 241 65 70 75 80
 243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 244 85 90 95
 246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 247 100 105 110
 249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 250 115 120 125
 252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
 253 130 135 140
 255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 256 145 150 155 160
 258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
 259 165 170 175
 261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
 262 180 185 190
 264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Gln Lys Phe

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:04

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

265 195 200 205
 267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
 268 210 215 220
 270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
 271 225 230 235 240
 273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
 274 245 250 255
 276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
 277 260 265 270
 279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
 280 275 280 285
 282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
 283 290 295 300
 285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
 286 305 310 315 320
 288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
 289 325 330 335
 295 <210> SEQ ID NO: 5
 296 <211> LENGTH: 51
 297 <212> TYPE: DNA
 298 <213> ORGANISM: Caenorhabditis elegans
 300 <400> SEQUENCE: 5
 301 tccattttctt ttgcgttaac cgtcgtcaact accatcgat acggtaatcc a 51
 304 <210> SEQ ID NO: 6
 305 <211> LENGTH: 51
 306 <212> TYPE: DNA
 307 <213> ORGANISM: Caenorhabditis elegans
 309 <400> SEQUENCE: 6
 310 tcattttctt ggtcgttcat tacaatgact actgtcggtt ttggcgactt g 51
 313 <210> SEQ ID NO: 7
 314 <211> LENGTH: 24
 315 <212> TYPE: PRT
 316 <213> ORGANISM: Drosophila melanogaster
 318 <400> SEQUENCE: 7
 319 Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
 320 1 5 10 15
 322 Arg Cys Val Thr Asp Glu Cys Pro
 323 20
 326 <210> SEQ ID NO: 8
 327 <211> LENGTH: 24
 328 <212> TYPE: PRT
 329 <213> ORGANISM: Drosophila melanogaster
 331 <400> SEQUENCE: 8
 332 Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
 333 1 5 10 15
 335 Arg Cys Val Thr Glu Gln Cys Ala
 336 20
 339 <210> SEQ ID NO: 9
 340 <211> LENGTH: 24

8/16, 0110 6

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<400> 65
Thr Trp Thr Phe
1

see item 11 on Env Summary Sheet

11

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001
TIME: 11:28:05

Input Set : A:\11420121.app
Output Set: N:\CRF3\06252001\H816011D.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1699 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: